

## S2 Table. Tools for RNA-seq analysis

All tools used in the online tutorial ([www.rnaseq.wiki](http://www.rnaseq.wiki)) are referenced below (in bold) along with alternative tools in each category. Where possible a citation is provided. Links are also provided to help the user evaluate the code and the level of maintenance. Where possible the link goes directly to a source controlled repository such as a git repo. Additional lists of tools can be found here: Alamancos et al. ([arXiv](#)), Hooper et al. [102], the [rna-seqblog](#), and [RNA-seq - Protocols and Algorithms](#). This table is meant to be comprehensive but not exhaustive. Some RNA-seq analysis applications that are not explicitly covered here include co-regulation (co-expression), disease classification, time series, expression compendium databases, outlier expression, data normalization, and miRNA analysis.

Category	Representative tools
Raw data QC [2, 103]	<a href="#">FastQC</a> , <a href="#">HTQC</a> [104], <a href="#">QC3</a> [105], <a href="#">KPAL</a> [106].
Read trimming [107]	<a href="#">Trimmomatic</a> [58], <a href="#">Skewer</a> [57], <a href="#">Flexbar</a> [108], <a href="#">FASTX</a> .
Alignment (splice aware, for alignment to a reference genome) [59]	<a href="#">TopHat</a> [84, 109], <a href="#">STAR</a> [110], <a href="#">HISAT</a> [111], <a href="#">segemehl</a> [112], <a href="#">GSNAP</a> , <a href="#">MapSplice</a> [113], <a href="#">JAGuaR</a> [114], <a href="#">SpliceMap</a> [115], <a href="#">HMMSplicer</a> [116], <a href="#">TrueSight/UnSplicer</a> [117].
Alignment (non splice aware for alignment to a reference transcriptome) [118, 119]	<a href="#">BowTie</a> [120], <a href="#">Bwa</a> [121].
Post-alignment QC [59]	<a href="#">FastQC</a> , <a href="#">samtools</a> [56], <a href="#">QuaCRS</a> [122], <a href="#">RSeQC</a> [123], <a href="#">RNA-SeQC</a> [124], <a href="#">Picard CollectRnaSeqMetrics</a> , <a href="#">BAMstats</a> , <a href="#">SAMstat</a> [125], <a href="#">BlackOPs</a> [126], <a href="#">seqbias</a> [127].
Gene/transcriptome annotation [128, 129]	<a href="#">AnnoScript</a> [130], <a href="#">XSAnno</a> [131], <a href="#">GeneMark-ET</a> [132], <a href="#">WIMpiBLAST</a> [133], <a href="#">RNASEG</a> [134], <a href="#">TSSAR</a> [135], <a href="#">Vicinal</a> [136], <a href="#">OMIGA</a> [137], <a href="#">CoRAL</a> [138], <a href="#">AfterParty</a> [139], <a href="#">ShortStack</a> [140], <a href="#">CIRI</a> [141].
Small RNA identification and characterization (e.g., miRNAs) [129, 142]	<a href="#">ShortStack</a> [140], <a href="#">CoRAL</a> [138], <a href="#">MTide</a> [143], <a href="#">FlaiMapper</a> [144], <a href="#">miRPlant</a> [145], <a href="#">PROMiRNA</a> [146], <a href="#">omiRas</a> [147], <a href="#">DREAM</a> [148].
Transcript assembly (reference genome guided) [60, 92, 149]	<a href="#">Cufflinks</a> [8], <a href="#">Scripture</a> [150], <a href="#">StringTie</a> [151], <a href="#">bayesembler</a> [152], <a href="#">IsoLasso</a> [153].

Transcript assembly ( <i>de novo</i> , reference genome free) [60, 149, 154-158]	<a href="#">Trinity</a> [159], <a href="#">Trans-ABYSS</a> [9], <a href="#">Oases</a> [160], <a href="#">RSEM</a> [161], <a href="#">DETONATE</a> [11], <a href="#">SEECER</a> (sequencing error correction for assembly) [162], <a href="#">BRANCH</a> [163] (uses partial or related genomics sequences as a guide), <a href="#">EBARDenovo</a> [164], <a href="#">Bridger</a> [165].
Transcript abundance or expression estimation (FPKM/RPKM) [91-94]	<a href="#">Cufflinks</a> [8], <a href="#">eXpress</a> [166], <a href="#">RSEM</a> [161], <a href="#">Sailfish</a> (alignment free) [167], <a href="#">RNA-Skim</a> (alignment free) [168], <a href="#">MITIE</a> [169], <a href="#">ireckon</a> [170], <a href="#">DRUT</a> [171].
Obtaining raw transcript/gene read counts (FPM/RPM) [17]	<a href="#">HTSeq</a> [172], <a href="#">FeatureCounts</a> [173], <a href="#">Rcount</a> [174], <a href="#">maxcounts</a> [175], <a href="#">FIXSEQ</a> (adjusts counts to compensate for overdispersion) [176], <a href="#">Cuffquant</a> .
Differential expression [67-69, 177]	<a href="#">Cuffdiff</a> [14], <a href="#">limma</a> [178], <a href="#">DESeq2</a> [179], <a href="#">EdgeR</a> [180], <a href="#">Corset</a> (for <i>de novo</i> assembled transcriptomes) [181], <a href="#">sSeq</a> [182], <a href="#">BADGE</a> [183], <a href="#">compcodeR</a> [184], <a href="#">metaRNASeq</a> [185], <a href="#">Characteristic Direction</a> [186], <a href="#">NPEBseq</a> [187].
Alternative splicing, alternative expression [94, 102, 188-191]	<a href="#">Cuffdiff</a> [14], <a href="#">DEXSeq</a> [192], <a href="#">ALEXA-seq</a> [3], <a href="#">IUTA</a> [193], <a href="#">FineSplice</a> [194], <a href="#">PennSeq</a> [195], <a href="#">FlipFlop</a> [196], <a href="#">SNPlife</a> [197], <a href="#">spliceR</a> [198], <a href="#">GESS</a> [102], <a href="#">RNASeq-MATS</a> [199], <a href="#">SplicingCompass</a> [200], <a href="#">DiffSplice</a> [201], <a href="#">SigFuge</a> [202], <a href="#">SUPPA</a> [bioRxiv], <a href="#">CLASS</a> [bioRxiv], <a href="#">SplAdder</a> [bioRxiv], <a href="#">SplicePie</a> [203].
Variant (e.g., SNP) and mutation detection [31-33] (germline or somatic) and eQTL/sQTL characterization [204]	<a href="#">GATK (Best Practices Guide)</a> [205], <a href="#">samtools</a> [56], <a href="#">SNVMix</a> [206], <a href="#">SNPlife</a> [197], <a href="#">eSNV-detect</a> [207], <a href="#">RVboost</a> [208], <a href="#">sQTLseekeR</a> [209], <a href="#">eQTL/ASE</a> , [BioRxiv], <a href="#">SNiPloid</a> [210], <a href="#">SNPiR</a> [32], <a href="#">QualitySNPng</a> [211], <a href="#">RNAmapper</a> [212], <a href="#">CRAC</a> [213], <a href="#">RADIA</a> [214].
RNA editing [21, 215-217]	<a href="#">REDItools</a> [218], <a href="#">GIREMI</a> [219], <a href="#">ICEBreaker</a> [220].
Allele specific expression [221-223]	<a href="#">AlleleSeq</a> [19], <a href="#">Allim</a> [224], <a href="#">mamba</a> [225], <a href="#">EMASE</a> , <a href="#">MBASED</a> [226], <a href="#">limma</a> [178].
Viral detection [23-25]	<a href="#">VirusSeq</a> [227], <a href="#">VirusFinder</a> [228], <a href="#">RNA CoMPASS</a> [229].
Fusion detection [26-30]	<a href="#">FusionQ</a> [27], <a href="#">TRUP</a> [230], <a href="#">Dissect</a> [231], <a href="#">Trans-ABYSS</a> [9], <a href="#">PRADA</a> (RNA-seq pipeline with a fusion module) [232], <a href="#">Pegasus</a> (used for fusion annotation) [233], <a href="#">FusionCatcher</a> , <a href="#">ChimeraScan</a> [234], <a href="#">TopHat-fusion</a> [235], <a href="#">BreakFusion</a> [236], <a href="#">deFuse</a> [237], <a href="#">FusionHunter</a> [238], <a href="#">EricScript</a> [239], <a href="#">Barnacle</a> [240], <a href="#">bellerophontes</a> [241], <a href="#">Chimera</a> (merge results from multiple fusion algorithms) [29], <a href="#">GFML</a> (format for representing fusion data) [242].

Visualization [243, 244]	<a href="#">SplicingViewer</a> [245], <a href="#">IGV</a> [62], <a href="#">Sashimi plots</a> [65], <a href="#">IGB</a> (splicing visualization protocol) [243], <a href="#">PrimerSeq</a> (Visualize RNA-seq data for primer design) [246], <a href="#">ASTALAVISTA</a> [247], Circos [248], <a href="#">Epiviz</a> [249], <a href="#">RNAbrowse</a> [250], <a href="#">ZENBU</a> [251], <a href="#">RNAseqViewer</a> [252], <a href="#">viRome</a> [253], <a href="#">miRseqViewer</a> [254], <a href="#">Circleator</a> [255], <a href="#">RNASEqBrowser</a> [256].
Integration of DNA-seq and RNA-seq data [257]	<a href="#">Veridical</a> [258], <a href="#">SpliceFinder</a> [259], <a href="#">nFuse</a> [260], <a href="#">RADIA</a> [214].